Expansion: A Novel Mutation Operator for Genetic Programming

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Abstract: Expansion is a novel mutation operator for Genetic Programming (GP). It uses Monte Carlo simulation to repeatedly expand and evaluate programs using unit instructions, taking advantage of the granular search space of evolutionary program synthesis. Monte Carlo simulation and its heuristic search method, Monte Carlo Tree Search has been applied to Koza-style tree-based representation to compare results with different variation operations such as sub-tree crossover and point mutation. Using a set of benchmark symbolic regression problems, we prove that expansion have better fitness performance than point mutation, when included with crossover. It also provides significant boost in fitness when compared with GP using only crossover on a diverse problem set. We conclude that the best fitness can be achieved by including all three operators in GP, crossover, point mutation and expansion.

1 INTRODUCTION

Genetic Programming (GP) is a stochastic generate-and-test approach to inductive program synthesis (Krawiec, 2016). Monte Carlo Tree Search (MCTS), also being a stochastic search method is yet to be effectively applied to evolutionary program synthesis (White et al., 2015) (Lim and Yoo, 2016). GP search space is extremely granular while the fitness landscape is exceptionally multi-modal. MCTS could take advantage of this granularity if every level of this search tree expands a unit instruction set. Traversing a tree made of programs using Monte Carlo Simulation can provide interesting advantages to program expansion with increased fitness.

2 PROGRAM SYNTHESIS

The earliest and the most commonly used method of program synthesis is the evolution of a tree structure of programs. Here representation is made using variable-length expressions from a functional programming language, like symbolic expressions (S-expr.) in LISP (Koza, 1992). Tree-based genetic programming (TGP) is the classic approach to GP where inner nodes of program trees hold functions (instructions) while leaves hold terminals which are input variable or constants.

When evolving programs are represented using computational nodes in a Cartesian coordinate system, the method can aptly be named *Cartesian Genetic Programming (CGP)* (Miller, 2011). It was first used by Miller for evolving digital circuits (Miller et al., 1997), but later became a general form of program evolution (Miller and Thomson, 2000). This representation can also be considered as a directed acyclic graph. Its genotypes are integers containing a node's input data source, operation and output destination. The genotype passes through a decoding process to result in an evolved program, which is its phenotype.

In Linear Genetic Programming (LGP) (Brameier and Banzhaf, 2010) the term *linear* refers to the structure of the program representation. Here programs in a population are represented as a sequence of instructions from an imperative programming language or machine language (Nordin et al., 1999). The main motivation of using a linear structure in LGP is the linear representation of the DNA molecule. Just as the DNA is divided into gene codes, a linear representation of a program can be divided into instructions, where each line of a single instruction is analogous to a gene.

The most obvious challenges to robust and scalable program synthesis, identified by Krawiec, is

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the size of the search space, its multimodal fitness landscape, externalized semantics of instructions and their complex interactions (Krawiec, 2016). In his recent study he identifies scalar evaluation of programs, which is the normalized count of successfully passing test cases, as a bottle neck. To solve this problem, he defines program semantics as a vector of program outputs for particular tests, providing more information about program behaviour than conventional scalar evaluation. The origin of Semantic Genetic Programming (SGP) comes from the belief that to scale evolutionary program synthesis, the algorithm needs to take program semantics into account (Krawiec and Lichocki, 2010). Also if we can exploit the geometry of its semantic space, it is possible to come up with more efficient search methods. The key intuition for Geometric Semantic Programming (GSGP) (Moraglio et al., 2012) focuses specifically on the geometric (metric-related) properties of program semantics. With this in mind different crossover operators such as Approximate Geometric Crossover (KLX) (Krawiec and Lichocki, 2009) and exact geometric crossover (GSGX) are defined (Krawiec, 2016).

Despite all the different methods using varied representations and variation operators, evolutionary program synthesis is still not efficient enough for practical software development. GP can only solve elementary small problems using enormous computational effort. Most of this effort is spent on the multitude of evaluations required on all different combinations of programs. It is imperative for GP to be more efficient in finding the optimum program with fewer evaluations.

3 MONTE CARLO TREE SEARCH

Monte-Carlo simulation is a highly effective method which depends on repeated random sampling. Monte Carlo Tree Search (MCTS) is a heuristic search algorithm which uses Monte-Carlo simulation to evaluate the nodes of a search tree. As a new paradigm for search, MCTS (Coulom, 2007b), has revolutionised not only computer Go (Gelly and Silver, 2011) (Coulom, 2007a), but also General Game Playing (Finnsson and Björnsson, 2008), Amazons (Lorentz, 2008), Line of Action (Winands and Björnsson, 2010), multi-player card games (Sturtevant, 2008) and real time strategy games (Balla and Fern, 2009). Replacing other traditional search methods, MCTS uses self-play, by simulating thousands of random games from its current position in the tree. Ideally an MCTS algorithm for game playing will contain the following four steps (Chaslot et al., 2008).

Selection. Selection is the process of selecting children of any node of the tree. Selection of the children provides for balance between exploration and exploitation of the search tree. Any method which can be applied for sampling can also be used for node child selection, depending on the problem being solved.

Expansion. This is the decision process of whether a node's children will be expanded for evaluation or not. For game playing the simplest strategy is to expand one node per simulated game (Coulom, 2007b). This step can be performed before or after simulation.

Simulation. For Go players this is the step where players play pseudo random moves of self play until the end of the game. Interesting moves and patterns are applied, to come up with game strategies. It is difficult to come up with an efficient strategy, to balance between *exploration* and *exploitation*. Having a strategy too stochastic results in weak moves where the level of Monte-Carlo program decreases. In contrast, having a deterministic strategy increases exploitation, which also decreases the level of Monte-Carlo program (Chaslot et al., 2008).

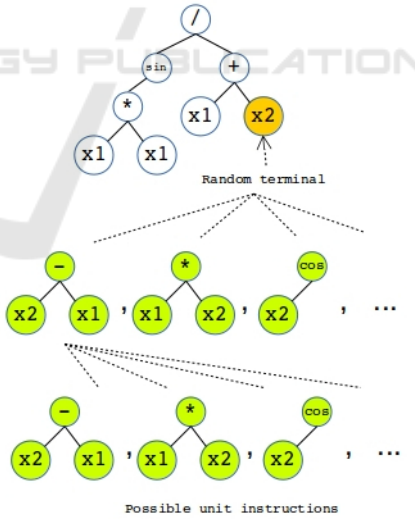


Figure 1: Monte Carlo Tree of Programs.

Backpropagation. This is the step in which results are propagated backwards from the leaf node. For the game of Go it could be the penalty of losing the game, or reward of winning it. A ratio of this win/loss value will be propagated backwards, to update its parent nodes about the outcome of this path.

3.1 Monte Carlo Tree of Programs

The Monte Carlo Tree (MCT) of programs can be defined using the definition of a *unit instruction*.

Unit Instruction. A unit instruction consists of a single operator (+, -, /, cos, log, etc.) and its operands (x, y, z, etc.). Here the number of operands depends on whether the instruction is unary or binary. The list of possible unit instructions consist of all combination of operators with all possible operands that can be attached to that operator.

We define an MCT of programs consisting of nodes similar to that of MCTS, where each node is a program (Figure 1). For MCT the root node is the initial program. **Expansion** is a mutation operator where the parent program that is selected for mutation is the root node of the MCT. The first level of this tree, right after the root node consists of the possible ways the root node can be expanded using a *unit instruction*. So each node of this level is a program expanded from the initial program by one unit instruction. The next level of MCT of programs consist of all possible ways the programs of the first level can be expanded using one unit instruction. Defined in the following section, the Expansion mutation operator simply traverses this MCT to find the best possible extension for the parent program.

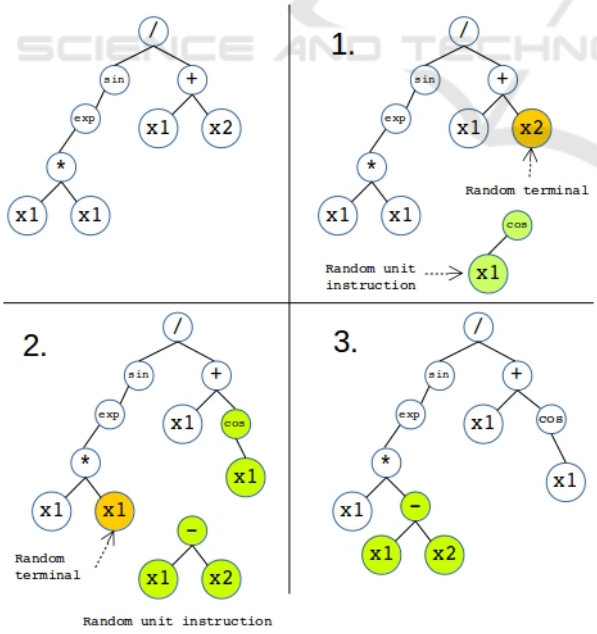


Figure 2: Program expanded with Monte Carlo Tree using a single simulation with a depth of 2.

3.2 Expansion: The Mutation Operator

Expansion, the mutation operator can be defined using the following terms.

Single Step Expansion. A single step expansion starts by selecting a random terminal from the s-expression of the initial program. Then a unit instruction is randomly selected from the list of possible unit instructions (Figure 2 step 1). Both of these processes perform uniform random selection. The selected terminal is then replaced by the unit instruction expanding the s-expression (Figure 2 step 2). For the next single step expansion this new expanded program is passed as the initial program (Figure 2 step 3).

Algorithm 1: Expansion using Monte Carlo simulation.

```
1:  procedure SIMULATE(currentIndividual, bestIndividual)
2:      for 1 to noOfSimulation do
3:          randomDistance ← random no. between 1 and maxDistance
4:          Create rootNode using currentIndividual
5:          simulateRecursive(rootNode, randomDistance)
6:      end for
        return list of betterNewIndividuals
7:  end procedure
8:  procedure SIMULATERECURSIVE(node, depth)
9:      if depth = 0 then
10:         evaluate(node.program)
11:     else
12:         Create childNode
13:         childNode.program ← clone of node.program
14:         terminalList ← findTerminals(childNode.program)
15:         randomTerminal ← select random terminal from terminalList
16:         Grow/Create random unit newGPnode
17:         newGPnode.parent ← randomTerminal.parent
18:         childrenList ← children of randomTerminal.parent
19:         Replace randomTerminal with newGPnode in childrenList
20:         evaluate(childNode.program)
21:         simulateRecursive(childNode, depth − 1)
22:     end if
23: end procedure
24: procedure EVALUATE(node)
25:     node.fitness ← Evaluate fitness by executing test cases
26:     if node.fitness > bestIndividual.fitness then
27:         Add node to list of betterNewIndividuals
28:     end if
29: end procedure
```

Single Simulation. A single simulation consists of one or more single step expansions to the parent program. *Maximum depth* of expansion is a constant defined as a parameter for the algorithm. Initially a random depth is generated between one and the maximum depth. For one simulation, starting from the parent program, the algorithm recursively keeps executing single step expansions up to that depth constraint.

In this way the algorithm performs a constraint *number of simulation*, also defined as a constant parameter at the beginning of the execution (Algorithm 1, Table 1).

The parent selection process for the *expansion* mutation operator is made using tournament selection. Once a parent is selected using a tournament, the algorithm also sorts the current population of programs by fitness, selecting the current best program in the population. Two constraints are passed to the algorithm as constant parameters. One is the *maximum depth* of expansion, while the other is the *number of simulations*. Using the parent program the algorithm starts performing simulations (Algorithm 1). At each single step expansion of each simulation the newly expanded program is evaluated for fitness. If the fitness for the new program is better than the best program in the population then it is added to a list of better programs. Once the algorithm completes all the simulation, the list of better new programs are sorted by fitness from which the best new program replaces the parent (Algorithm 2).

It is worth mentioning that the new programs generated by *expansion*, are compared with the current best in the population, instead of their own parent as this method maintains diversity in the entire GP population. If we compare with the current parent, there will be more individuals added by *expansion* to the population in each generation, reducing diversity.

Thus we can observe that MCTS can effectively be applied to program expansion. *Expansion*, the new mutation operator, is inspired by MCTS. Each step of MCTS is reflected in this algorithm. It uses uniform random for **selection** of (MCT) nodes to expand. After selection **simulations** are performed using a series of **expansions**. Once all the simulation is complete, the algorithm **backpropagates** to the initial program only to attach the extension from all the simulation which provided the best fitness.

4 ECJ: EVOLUTIONARY COMPUTATION LIBRARY

The Evolutionary Computation Library in Java (ECJ) (Luke, 1998) is one of the oldest open source, unified metaheuristic toolkits, with strength in the implementation of Genetic Programming (GP) (Luke, 2017). The evolving architecture and support of ECJ has played a pivotal role in making it a widely used library for experimenting almost any algorithm in evolutionary computation. Its flexible object oriented design is very easy to extend and customize. Also it is written in the most widely used object oriented language, Java. ECJ's GP implementation is influenced by John Koza's *Genetic Programming* (Koza, 1992) and succeeding texts. Also Koza's "Simple Lisp" has been used as the programming language for GP evolution in ECJ. That is why ECJ's Koza-style implementation of Genetic Programming has been used for evaluating the performance of the *Expansion* mutation operator.

Algorithm 2: Expansion pipeline.

```
1: procedure PRODUCE
2:     individual ← Grab random individual from Reproduction Pipeline
3:     bestIndividual ← Find current best individual from the population
4:     betterNewIndividuals ← simulate(individual, bestIndividual)
5:     bestNewIndividual ← best from list of betterNewIndividuals
6:     replace individual with bestNewIndividual
7: end procedure
```

ECJ's top level evolutionary loops are designed for execution of any evolving algorithm. It is a simple loop over *individuals* in a *population* with steps of *initialization*, *evaluation*, *breeding*, *exchanging* and finally *terminating*, when the algorithm reaches the maximum number of generations or best fitness evaluation.

In ECJ, the structure and operation of an experiment is defined using a set of parameter files, where the *Problem* is written by the researcher. Using simple scripting with the parameter files, it is possible to make major architecture change in the execution of the evolving algorithm. In this library the population contains a set of sub-populations, which can be evolved independently and also asynchronously. This can be helpful for algorithms involving co-evolution or island models.

Each individual in ECJ contains a representation and fitness both of which can have many variations. For generational breeding, the experimenter is supposed to specify one or more *Breeding Pipelines*, which is a combination of selection, mutation and recombination procedures. These processes define an individual's method of selection, copy, modification and addition into a new population.

Genetic Programming in ECJ. Originally designed for GP, ECJ implements the Koza-style GP using trees of nodes. Each *GPIndividual* object contains forests of *GPTree*, which in turn holds a tree of *GPNodes*. Using a set-based Strongly-Typed Genetic Programming, each node's parent and child slots are augmented with a set of types. Similar is the case for the tree's root slot. Parent slots may attach to other node's child slots, or to the tree's root slot, given their two set's intersection is nonempty.

4.1 Crossover Pipeline

Being a subclass of *GPBreedingPipeline*, *Crossover-Pipeline* performs strongly-typed version of Koza-style "Subtree Crossover". After selecting two random individuals (Figure 3), a single tree is chosen from each individual having similar *GPTreeConstraints*, meaning their tree type, builder and function set are the same. The selection of random nodes in each tree is done making sure that each node's return type is compatible with the argument type of the parent's slot which contains the other node. Also if this swap exceeds the maximum depth constraint, the entire operation is discarded and repeatedly tried again to a constrained number of times. If a successful crossover fails to occur, within that limited number then the two individuals are 'reproduced' to the new subpopulation without any change. For the work presented in the paper, no change was made to the default ECJ implementation and parameters of crossover.

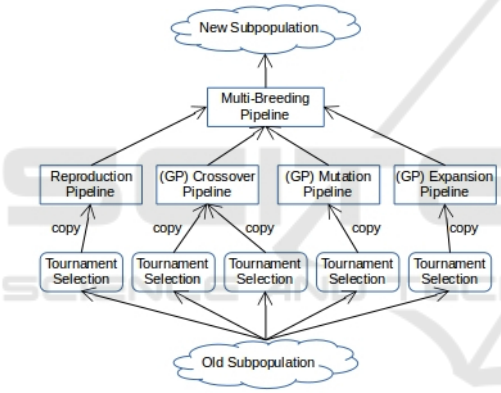


Figure 3: GP Pipelines including expansion. Diagram extended from (Luke, 2017)

4.2 Mutation Pipeline

Koza's definition of *Point Mutation* (Koza, 1992) begins by selecting a point at random within the tree which could be a terminal or a non-terminal. A randomly generated subtree is inserted at that point after removing whatever is currently there at that point. In ECJ, *MutationPipeline* is another type of *GPBreedingPipeline* which implements a strongly-typed version of the point mutation. In addition it provides a depth restriction where if the tree becomes larger than a maximum depth, it is discarded, while the process is repeated until satisfying this constraint. Similar to crossover (Section 4.1), if the number of repeat constraints is violated, then the individual is reproduced to the new population as it is. The default ECJ implementation and parameters of this process were not changed for any experiments for the research presented in the paper.

4.3 Expansion Pipeline

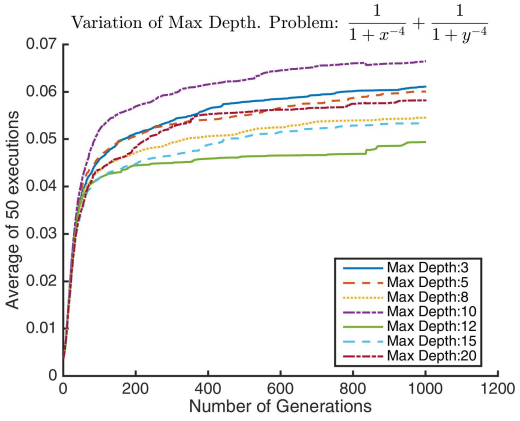
The *ExpansionPipeline* is also an extension of the *GPBreedingPipeline*, and is the primary contribution of this paper. The process is described in Algorithm 2. An individual is selected using ECJ's default Tournament Selection, which is also used for both the crossover (Section 4.1) and mutation (Section 4.2) pipelines. After sorting the current sub-population, the current best individual is also picked. Using the selected individual a simulation is performed with MCT (Section 3.1), which executes randomized single step expansion and evaluation on randomly selected terminals of the tree. Each simulation is performed up to a maximum depth for a certain number of times (*max depth* and *no. of simulation* in table 1). This simulation and expansion process is explained in detail using algorithms 1 and 2 (Section 3.2). As each unit expansion is evaluated, the new individual's fitness is compared with the fitness of the best individual in the sub-population. If better, it is added to a list of better individuals. Once simulations are complete the list of better individuals are again sorted to come up with the best from that list, which replaces the original individual picked from the population.

5 EXPERIMENTS AND RESULTS

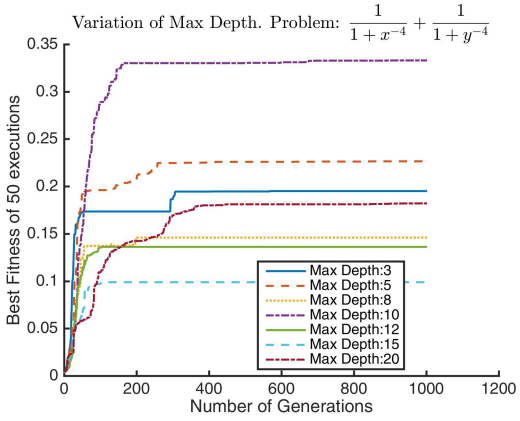
Before our discussion on the experimental procedure we describe the problem set that was used to find best possible comparison for expansion (Section 5.1).

5.1 Benchmark

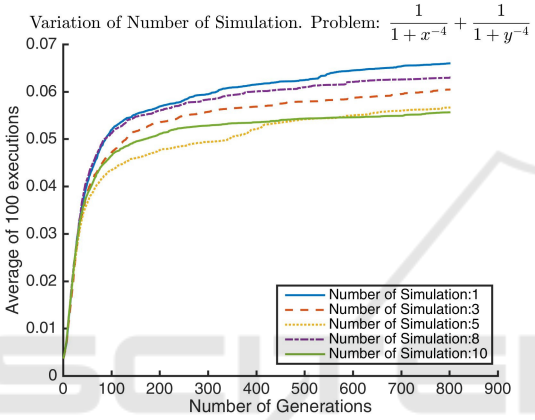
To avoid the simplicity of historically used GP problems and to tackle real world complexities, (McDermott et al., 2012) and (White et al., 2013) suggested a set of benchmark problems which is currently considered a standard for evaluating any version of GP algorithms. The benchmark problem set has the characteristics of being difficult to choose, varied, relevant to the field, fast to execute, easy to interpret and compare while being precisely defined. From the different type of problems (regression, classification, predictive modeling, etc) that received consensus of the research community, a variety of symbolic regression problems have been used in this research to evaluate performance of *expansion*, as a mutation operator. Out of the 53 symbolic regression problems (McDermott et al., 2012), Pagie-1 ($\frac{1}{1+x^{-4}} + \frac{1}{1+y^{-4}}$) has the re-



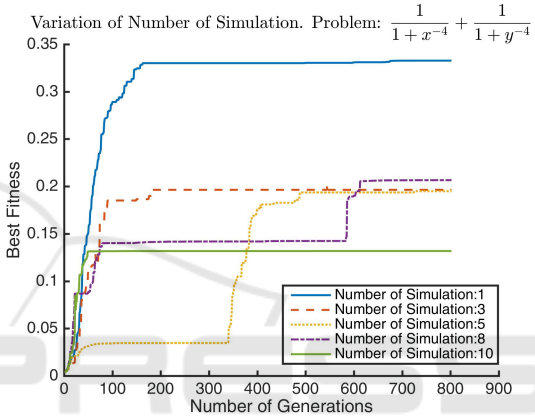
(a) Variation of *max depth* - avg. of 50 executions



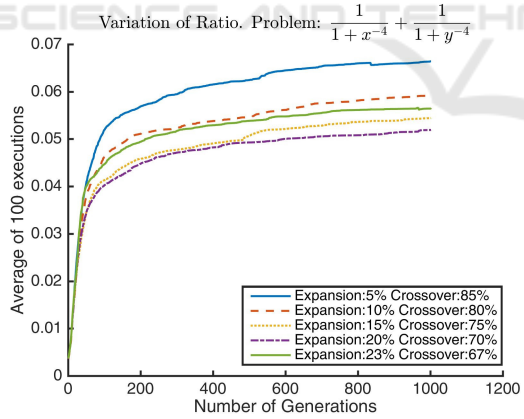
(b) Variation of *max depth* - best of 50 executions



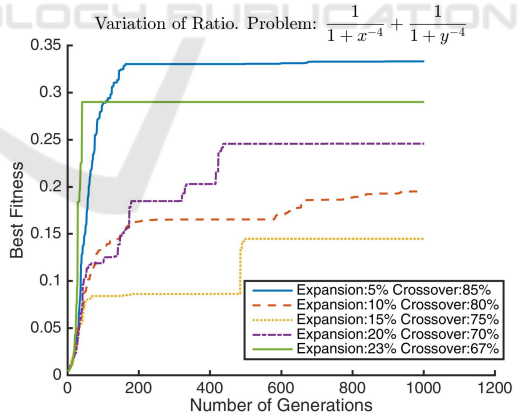
(c) Variation of *no. of simulation* - avg. of 100 executions



(d) Variation of *no. of simulation* - best of 100 executions

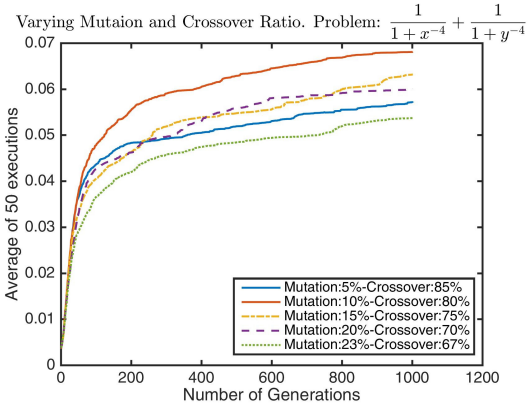


(e) Varying ratio of expansion - avg. of 50 executions

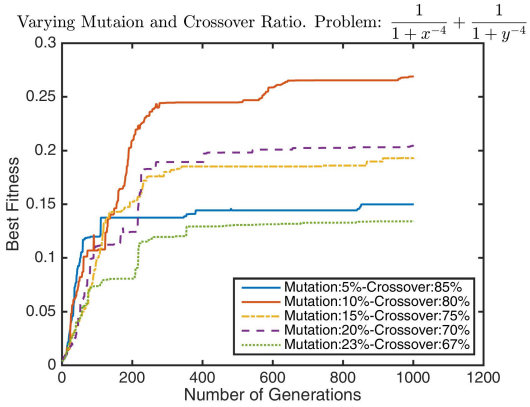


(f) Varying ratio of expansion- best of 50 executions

Figure 4: Comparison of different parameters and ratio of *Expansion*. In the above graphs the horizontal axis contain number of generation, while the vertical axis is the Koza fitness of the best individual in the population in that generation. (a, c, e) contain average of 50 executions, while (b, d, f) contain the best run of 50 executions. (a, b) compare the *Maximum Depth* parameter varying from 3 to 20. Without any apparent pattern we can observe *Maximum depth* 10 has the best overall fitness. In (c, d) we compare the *Number of Simulation* parameter varying from 1 to 10, where the value of 1 seem to provide the best result. (e, f) tell us the best ratio of Expansion with Crossover, where we find only 5% expansion provides the optimum output. These graphs also did not following any obvious pattern. Problem source: (Pagie and Hogeweg, 1997).



(a) Variation of Mutation ratio - avg. of 50 executions



(b) Variation of Mutation ratio - best of 50 executions

Figure 5: Comparison of different Point Mutation (Section 4.2) and Crossover (Section 4.1) Ratio. In the above graphs the horizontal axis contain number of generation, while the vertical axis is the Koza fitness of the best individual in the population in that generation. (a) contains average of 50 executions, while (b) contains the best run of 50 executions. We can observe without any apparent pattern 10% of Point Mutation performs best with 80% of Crossover.

putation of being particularly challenging (Pagie and Hogeweg, 1997), as it has a rugged fitness landscape and limited number of possible solutions. That is why Pagie-1 has been used for the comparison study of different parameter variation for expansion (Section 5.3, 5.4). After selecting reasonably best parameters, a comparison study has been done on other diverse problems from the benchmark (Section 5.6). ECJ has a complete implementation of all the Benchmark problems, optimized using the Reproduction, Crossover (Section 4.1) and Mutation (Section 4.2) pipelines. For this study ExpansionPipeline was added to ECJ and its best ratio was compared with crossover and mutation.

Koza Fitness. Described in (Koza, 1992), Koza fitness is a fitness measure used in ECJ to normalize the error rate of the benchmark symbolic regression problems. Here fitness $f = 1/(1+e)$, where e is the summation of the errors from all the tests. All results presented in this paper use this measure of fitness.

5.2 Experimental Procedure

Program expansion using MCT is most effective when it is used along with the crossover (Section 4.1) and mutation (Section 4.2) pipeline in ECJ. Executing GP using only expansion did not provide a competitive result. All experiments in the following sections were done up to 1000 generations. The average fitness curves were generated from 50 consecutive executions. For comparison (Section 5.6) problems from (Keijzer, 2003) and (Vladislavleva et al., 2009) were selected as they were difficult enough not to reach their best fitness within 1000 generations. ECJ ReproductionPipeline which is a type of breeding pipeline that simply makes a copy of the individuals it receives from its source (Figure 3) maintains a constant ratio of 10% in all the experiments (Table 1). Complete source code of the ExpansionPipeline, parameters and results associated to experiments presented in this paper can be found at (Islam, 2018).

5.3 Expansion Parameters

To evaluate performance of the ExpansionPipeline, the initial experiments were designed to find the relatively optimum point of its two significantly important parameters *maximum depth* and *number of simulation* (Figure 4 a,b,c,d).

Using one of the most difficult problems from benchmark, Pagie-1 (Pagie and Hogeweg, 1997) different depth variations were applied for the simulations performed (Figure 4 a,b). The other parameters for this experiment remained constant (ratio of expansion: 5%, crossover: 85%, no. of simulation: 1). Maximum depth was varied from 3 to 20 with different intervals where the best fitness performance was found at 10, for both the average and the best fitness of all 50 executions. These results are explained as follows: if the maximum depth of each simulation is too high, the search space of the programs in the population is larger, resulting in bad fitness. Also if the depth is too small then expansion has very little impact.

Similarly, number of simulation was varied between 1 to 10 in figure 4(c,d), were a single simulation seemed to have the optimum impact for increasing overall fitness in both average and best of 50 experiments.

5.4 Expansion Ratio

Once a reasonable parameter choice was found, the next step is to find the best ratio between expansion and crossover (Section 5.4). As compared in figure 4(e,f), the best fitness impact comes from very little expansion, only 5%. This can be explained as increasing the program size too quickly has negative impact on fitness performance. Because it also increases the size of the search space, it is harder for GP to find the optimum program.

5.5 Mutation Ratio

Expansion being a mutation operator, it is important that we compare it with other mutation operators, namely the most widely used Point Mutation by Koza (Koza, 1992) (Section 4.2). Before this comparison study, an experiment was done to find the best ratio between point mutation and crossover pipelines in ECJ. Figure 5 contains the average and best results of 50 executions where 10% point mutation rate along with 80% crossover seems to have the best impact in fitness.

5.6 Comparison

ECJ's default Koza-style GP implementation uses only crossover. So when we have the best ratio between expansion-crossover and mutation-crossover, the final comparison is done between only-crossover, expansion-mutation-crossover and the two above. Four GP variations (Table: 1) are executed 50 times on a variety of symbolic regression problems from the benchmark list (Section 5.1). These results are presented in figures 6, 7, 8. The problems were selected avoiding the ones which are too simple to reach their optimum fitness within 1000 generations. Algorithms with version 3 and 4 from Table 1 contain the best ratio of expansion with its reasonably optimum parameters (depth, no of simulation). They both start with a population of 1024, but due to the additional evaluations of every step of expansion, the average number of evaluations per generation increases to 1120. Version 1 and 2 is for only-crossover and mutation-crossover, where the population has been purposefully increased to 1120 so that the average number of evaluations per generation remains the same for all three versions of the algorithms. ECJ's implementation of a single execution of the CrossoverPipeline start with two randomly selected individuals, and ends in evaluating two new ones. MutationPipeline evaluates only one newly mutated individual. So without making any changes to the existing ECJ implementation, the only way to increase the number of evaluations for version 1 and 2 was to increase the population. Increasing the population also provides an added advantage to version 1 and 2 of the algorithms as it provides a larger search space for GP combinatorial search. This advantage is slightly less (population 1024) for version 3 and 4, were expansion is applied.

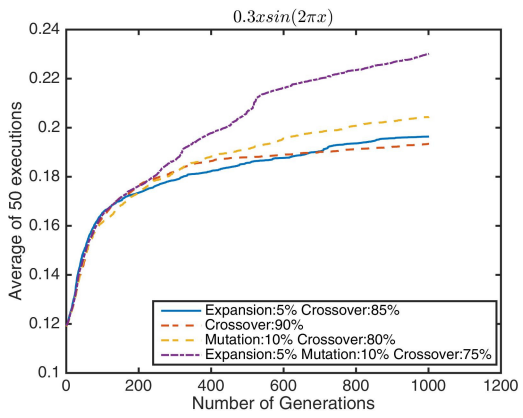
Table 1: Parameters for compared versions.

Version	Population	Reproduction	Crossover	Mutation	Expansion	Max Depth	Number of Simulation	Average number of Evaluations/Generation
1	1120	10%	90%	0	0	-	-	1120
2	1120	10%	80%	10%	0	-	-	1120
3	1024	10%	85%	0	5%	10	1	1120
4	1024	10%	75%	10%	5%	10	1	1120

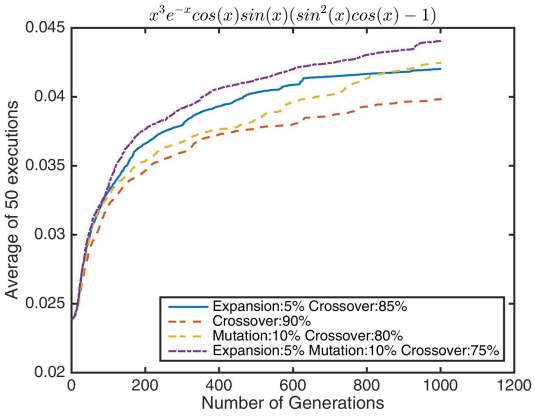
6 ANALYSIS

Analysing the comparison results of figures 6, 7, 8, we can observe that version 4 with expansion-mutation-crossover almost always provided the best fitness over 1000 generations of 50 executions. Version 3 with expansion-crossover is competitive with Version 2 which is mutation-crossover, where both of them have performed better than version 1, only-crossover. Overall Version 2 performs worse than version 3 and 4 (in most cases). This result was obtained after providing added advantage of an increased population to version 1 and 2, and having the same number of evaluations per generation for all four. A small ratio of expanding with unit instructions and fitness evaluation of each step of this process has a large impact in overall GP performance. In GP, crossover has always provided the highest impact as a variation operator (Koza, 1992). But we can observe from the comparison study that a little expansion can boost this performance significantly.

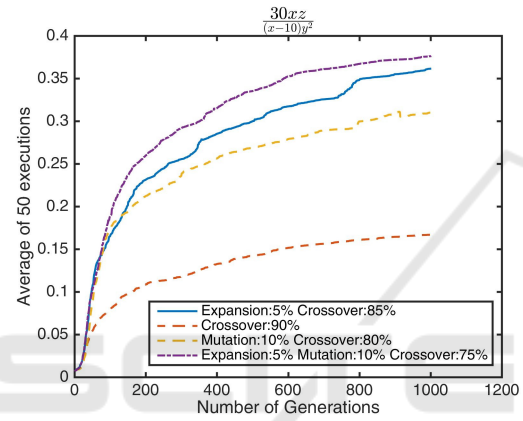
Expansion also performs better than point mutation. With number of simulation as 1 for expansion, their algorithmic difference is the step by step evaluation of each unit expansion, which does not happen to programs when point mutation is applied. *Expansion* as a mutation operator takes into consideration the granularity of programs at the level of unit instructions, which is lacking in point mutation, where sub-trees are added, replaced or removed.



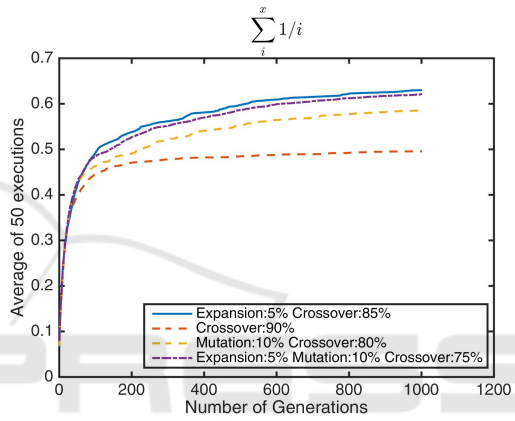
(a) keijzer2



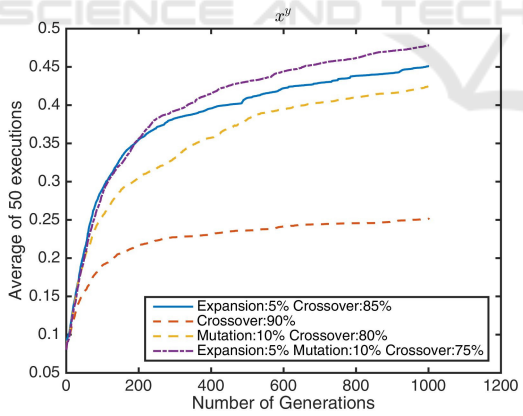
(b) keijzer4



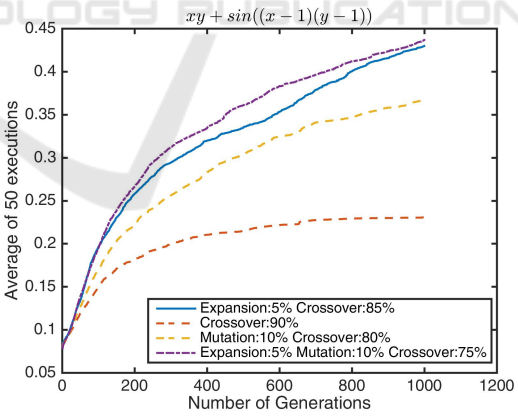
(c) keijzer5



(d) keijzer6

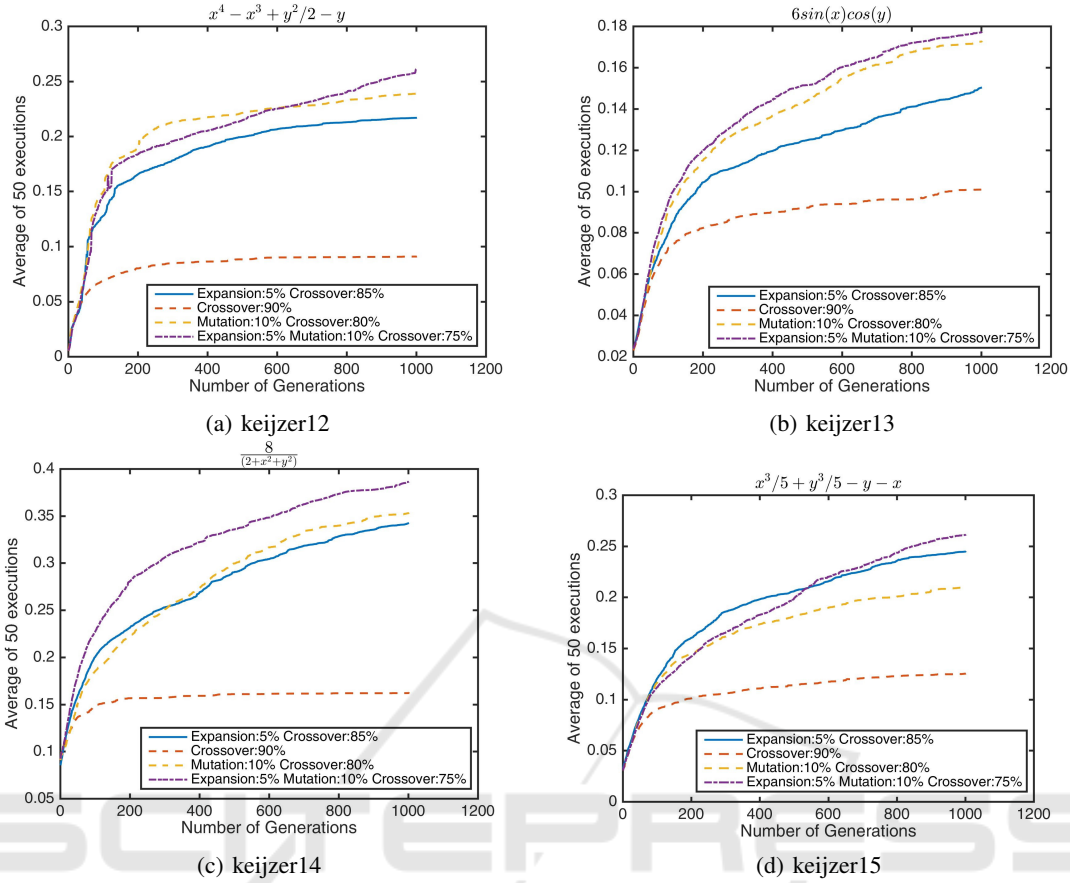


(e) keijzer10



(f) keijzer11

Figure 6: Comparison between Crossover, Mutation and Expansion Ratio. In the above graphs the horizontal axis contain number of generation, while the vertical axis is the Koza fitness of the best individual in the population in that generation. All these problems were picked from the benchmark list (McDermott et al., 2012), from which their names originate (keijzer 2,4,5, etc.). For all figures 5% *expansion* has provided a boost in performance. For (a, b, c, e and f) version 4 (5% *expansion*, 10% mutation and 75% crossover) was able to reach the best fitness. For (d) version 3 (5% *expansion* and 85% crossover) seems to be doing slightly better than version 4 (Keijzer, 2003).



(a) keijzer12 (b) keijzer13

(c) keijzer14 (d) keijzer15

Figure 7: Comparison between Crossover, Mutation and Expansion Ratio. In the above graphs the horizontal axis contain number of generation, while the vertical axis is the Koza fitness of the best individual in the population in that generation. The problem set is from the same source as figure 6 (Keijzer, 2003). Version 4 (5% *expansion*, 10% mutation and 75% crossover) has provided the best fitness is all cases.

7 CONCLUSION

Monte Carlo simulation has been an effective method in diverse fields (Eckhardt, 1987) (Benov, 2016). MCTS has created impact for problems involving large search space (Section 3). Combinatorial optimization techniques such as genetic programming is a search over an infinitely large space of combinations of programs. That is why we can apply MCTS in various new and effective ways to program synthesis. The mutation operator *expansion*, presented in this paper is only one of these ways. Using a comparison study with crossover and point mutation the effectiveness of the Monte Carlo method can be observed in program synthesis. The benchmark symbolic regression problems used in this study are considered as the community standard, with which we prove that expansion have a better fitness performance than point mutation when included with crossover. Also fitness is significantly boosted on a variety of problems when a small ratio of expansion is added to crossover and mutation, compared to GP using only-crossover and crossover-mutation. It is worth emphasising that for all cases the expansion algorithm achieves such improvement using the same number of fitness evaluations. Also we reach the conclusion that the best fitness can be achieved by including all three operators in GP, crossover, point mutation and expansion.

A study of the impact of program bloating is required on *expansion*, which is currently being done by the authors.

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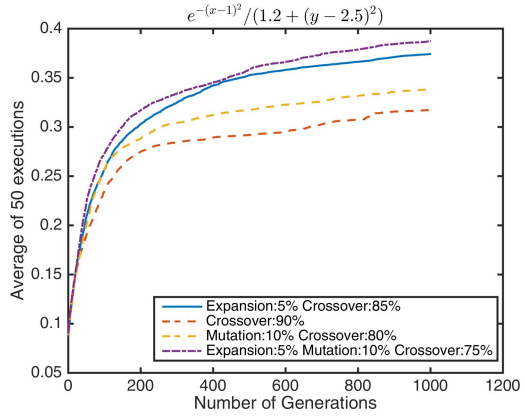

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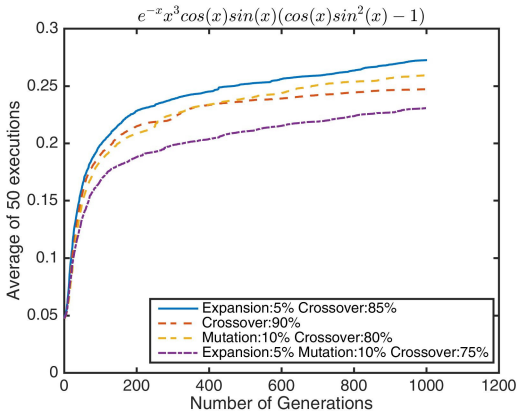
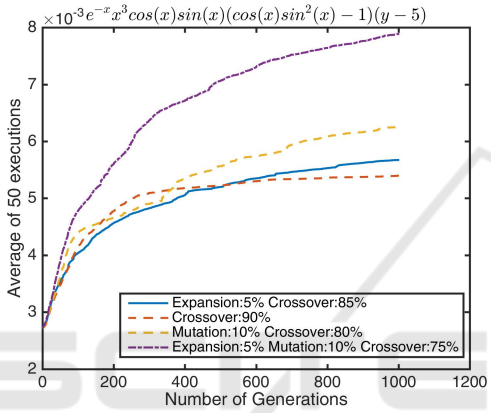
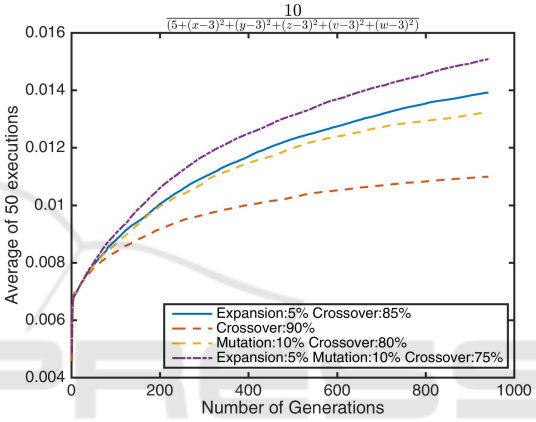


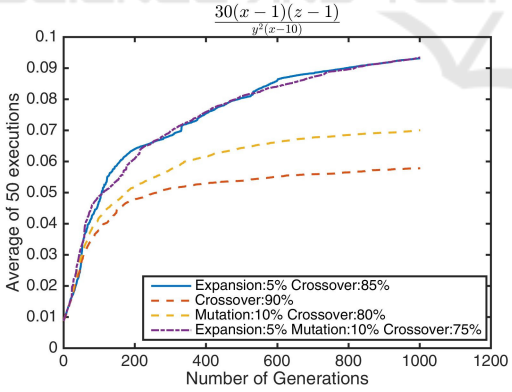
(b) vladislavleva2



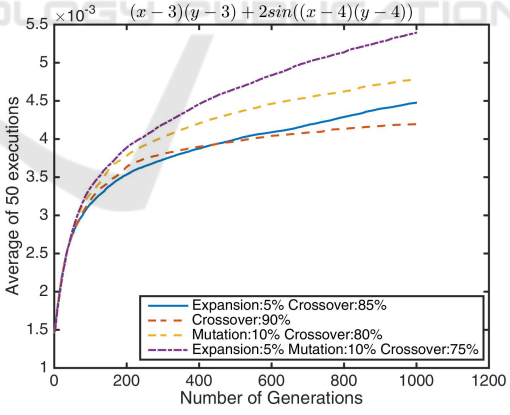
(c) vladislavleva3



(d) vladislavleva4



(e) vladislavleva5



(f) vladislavleva7

Figure 8: Comparison between Crossover, Mutation and Expansion Ratio. In the above graphs the horizontal axis contain number of generation, while the vertical axis is the Koza fitness of the best individual in the population in that generation. All these problems were picked from the benchmark list (McDermott et al., 2012), from which their names originate (vladislavleva 1,2,3, etc.). For all figures 5% *expansion* has provided a boost in performance. For (a, c, d, e and f) version 4 (5% *expansion*, 10% mutation and 75% crossover) was able to reach the best fitness. For (b) version 3 (5% *expansion* and 85% crossover) seems to be doing better than version 4 (Vladislavleva et al., 2009).

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